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Back to the past: “find the guilty bug—microorganisms involved in the biodeterioration of archeological and historical artifacts”

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BACK TO THE PAST. "FIND THE GUILTY BUG: MICROORGANISMS INVOLVED IN THE BIODETERIORATION OF ARCHEOLOGICAL AND HISTORICAL ARTEFACTS"

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ABSTRACT

Microbial deterioration accounts for a significant percentage of the degradation processes that occur on archeological/historical objects and artworks, and identifying the causative agents of such a phenomenon should therefore be a priority, in consideration of the need to conserve these important cultural heritage items. Diverse microbiological approaches, such as microscopic evaluations, cultural methods, metabolic- and DNA-based techniques, as well as a combination of the aforementioned methods, have been employed to characterize the bacterial, archeal and fungal communities that colonize art-objects. The purpose of the present review article is to report the interactions occurring between the microorganisms and nutrients that are present in stones, bones, wood, paper, films, paintings and modern art specimens (namely, collagen, cellulose, gelatin, albumin, lipids and hydrocarbons). Some examples, which underline that a good knowledge of these interactions is essential to obtain an in depth understanding of the factors that favor colonization, are reported. These data can be exploited both to prevent damage, and to obtain information on historical aspects that can be decrypted through the study of microbial population successions.

Key-words: stone deterioration, syntrophic chains, wood decay, motion picture and photographic film degradation, xenobiotic degraders, amino acid racemization

INTRODUCTION

Although exposure to physico-chemical agents can be responsible for the significant deterioration of objects of historical interest (especially outdoor objects), microbial degradation also plays a major role, due to the huge metabolic diversity of microbes and the high efficiency of the enzymes selected during evolution to ensure microbial survival in different environments. Most degradation pathways that occur on cultural heritage items are used by microorganisms for nutrition. On the other hand, metabolic products such as acids, solvents, surfactants, pigments and biofilms contribute to alter and damage artworks and archeological specimens.

Damage is sometimes caused by a predominant microbial group (e.g. the cellulolytic organisms involved in paper degradation). However, most of the time, there is a syntrophic chain in which several species contribute to a single sequenced deterioration step by releasing catabolites that become nutrients for further colonization. Identifying the microbial species involved in these complex deterioration phenomena is an essential pre-requisite for setting up rational prevention, conservation, *in situ* protection and restoration strategies. The most relevant literature data concerning the identification of the microbial species involved in the bio-deterioration of different substrates and artworks have been reported in the present mini-review.

Biodeterioration of stone, metal and glass material: the contribution of autotrophic organisms and syntrophic chains

Outdoor stone monuments, caves and crypts all suffer from microbial biodeterioration. According to Martino (2016), stone material suffers from three types of deterioration: 1) esthetic surface damage, such as biofilm or pigment production 2) chemical damage, such as acid production or microbial-induced salt crystallization, which can cause discoloration and erosion 3) structural damage due to the penetration of fungal hyphae into stone. The latter, apart from causing swelling, favors water and nutrient transport inside the stone, thus leading to further bacterial colonization (McNamara and Mitchell 2005). Laiz and co-workers (2003) monitored the bacterial colonization of stone monuments and found that culturing led to an overestimation of spore-forming bacteria, and pointed out that culture-independent methods should therefore be preferred.

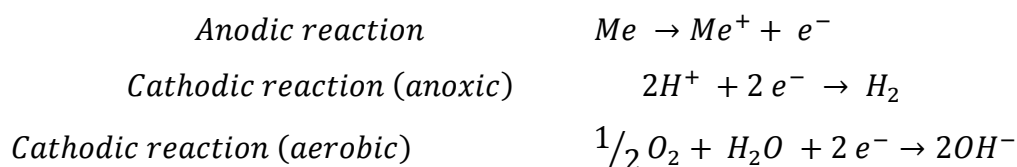
Autotrophic organisms may be the starters of syntrophic chains. Chemoautotrophs (such as the acid-producing sulfur-oxidizing and nitrifying bacteria that dissolve the alkaline material of stone) can be involved, but photoautotrophs, such as cyanobacteria, are better adapted to the oligotrophic and dry stone habitat. The latter can use K^+ and Ca^{2+} ions from the rock as nutrients. Halophylic archaea, such as *Halobacterium* and *Halococcus*, can grow in salty environments. They can grow, for

instance, on stone material which shows intrinsic or biologically-driven salt efflorescences. Moreover, they can sometimes produce pink pigments, such those observed in the Johannes chapel in Pürgg (Austria) (Ettenauer et al. 2014). Because of their adaptability to even low light intensity (Kehoe and Grossman 1994), Cyanobacteria (e.g. *Fisherella*, *Eucapsis*, *Leptolyngbya*) can colonize semi-dark environments like catacombs and the *Domus Aurea* hypogeal sites in Rome (Bellezza et al. 2003), as well as outdoor monuments such as the Propylaea columns in the Acropolis in Athens (Lamprinou et al. 2013). Cyanobacteria can penetrate into a stone and create small cavities that favor water retention, thus allowing the less desiccation-resistant algae to grow (Martino 2016). Algae are frequently involved in green pigmentations, regardless of the humidity of the site, when intense light is available (Cutler et al. 2013). Once Archaea, cyanobacteria and algae growth has become established, heterotrophic bacteria and fungi can appear. Autotrophs can in fact release extracellular organic matter (i.e. biofilm), which, together with dirty abiotic particles, dust, pollen, leaves, bird excrements, mineral elements of the stone itself and dead cell, can support the growth of nutritionally exigent heterotrophs. Phototroph/heterotroph mixed species biofilms, which are frequent on stone surfaces, chemically modify a microhabitat through interspecies interactions, and this leads to reciprocal nutrition and cross-feeding, thus gaining survival for the whole community in a very harsh environment (Villa et al. 2015).

Heterotrophic bacteria, such as *Sarcina*, *Micrococcus*, *Staphylococcus*, *Bacillus*, *Alcaligenes*, *Pseudomonas*, *Flavobacterium*, *Mycobacterium* and *Nocardia* can colonize stone monuments, but the predominant action is due to the filamentous *Actinobacteria*, which can utilize a wide range of carbon and nitrogen sources (Saarela et al. 2004). *Actinobacteria* of the *Geodermatophilaceae* family (especially *Blastococcus* and *Modestobacter*, which are well-adapted to light-induced oxygen stress) have been found in arid environments (Gtari et al. 2012), such as on stone monuments in the Egyptian and Tunisian deserts. They have been characterized and clustered by means of esterase profiling (Essoussi et al. 2010). The role of both epilithic and endolithic bacteria has been reviewed extensively by McNamara and Mitchell (2005). Mycelium bearing-fungi, such as *Alternaria*, *Aureobasidium*, *Cladosporium* and *Phoma*, prevail in humid environments, whereas small-colonies black fungi belonging to *Sarcinomyces*, *Coniosporium*, *Hortea*, *Knufia*, *Exophiala*, *Trimmatostroma* and *Capnobotryella*, are more frequently isolated in dry samples (granite, marble and limestone), and sometimes in association with lichens (Sterflinger 2010). The latter are better adapted to temperature and humidity variations and thus prevail in extreme habitats (Martino 2016). A very interesting study by Cappitelli et al. showed the presence of both green-black crusts and sulfatation in different areas of Milan Cathedral (Cappitelli et al. 2007). Culture-based investigations revealed the presence of both heterotrophic bacteria (average 10^6 CFU/g) and fungi (average 10^4 CFU/g), but the use of a molecular

approach (Fluorescence in situ hybridization, FISH) also detected Cyanobacteria and Archaea. This highly innovative method exploited adhesive tape strips for the sampling, thus also providing information on the spatial distribution of the different microbial genera, without altering or damaging the stone surface.

As far as microbial induced damage of metal antiquities (e.g. coins, weaponry and statues) is concerned, corrosion may result from chemical or biochemical redox reactions. Metal corrosion can be schematized as being composed of an anodic reaction, in which the metal is oxidized, and a cathodic reaction, in which another chemical species (generally H^+ or O_2 , depending on whether there are anoxic or aerobic conditions) is reduced:



Microorganisms can promote metal corrosion by accelerating an anodic or cathodic reaction, or even both (Videla and Herrera 2005). Microorganisms that consume H_2 generally enhance a cathodic reaction, whereas those producing acidic metabolites and/or secreting enzymes may accelerate metal oxidation (Kip and van Veen 2015). In the case of iron or steel artifacts, sulfate-reducing/sulfur-oxidizing bacteria, iron-oxidizing/iron-reducing bacteria and manganese oxidizers can act as corrosion agents (Kip and van Veen 2015). As for other inorganic materials, such as stone artifacts, metal bio-corrosion is generally the result of the activity of multi-species microbial communities embedded in biofilms (Videla and Herrera 2005). In these syntrophic chains, the role of heterotrophic species, such as *Clostridium* sp. or *Penicillium* sp. in metal corrosion cannot be neglected, since their metabolic products include both organic and inorganic acids, both of which can oxidize metals (Kip and van Veen 2015). Furthermore, the extracellular polymeric substances (e.g. exopolysaccharides, proteins, lipids) that constitute the matrix of biofilms are responsible for the metal/environment interface characteristics and can affect the electrochemical corrosion process to a great extent (Beech and Sunner 2004). The recent application of metagenomics techniques to study metal corrosion has in fact indicated that the microbial communities involved in this phenomenon are much more complex than previously thought (Marty et al. 2014; Oliveira et al. 2011). Furthermore, these researches have suggested that sulfate-reducing bacteria may not always be the main players in the bio-corrosion of metals.

Microbial-induced corrosion mainly concerns buried, sunk or poorly conserved metallic antiquities or artworks (Del Junco et al. 1992). Uncommon corrosion products, such as Mackinawite (FeS) or Greigite (Fe_3S_4), which are ascribable to the activity of sulfate-reducing bacteria, have been

122 detected for instance on archaeological iron items, such as Roman iron ingots and nails (Rémazeilles
 123 et al. 2010a; b). Archaeological copper artifacts and copper alloys (e.g. bronze) are also susceptible
 124 to the metabolic activity of sulfate-reducing bacteria (Ghiara et al. 2018). Evidence of microbial
 125 induced corrosion was found in tin-bronze decorative artifacts, greaves and swords dating back to
 126 between the 15th and 11th century B.C., which were found in different contexts in Austria, Bosnia and
 127 Croatia (Piccardo et al. 2013). As the result of the microbial induced corrosion of copper, a very
 128 resistant black patina, which is rich in sulfur, copper oxides, carbonates and/or hydroxy-chlorides, is
 129 formed (Ghiara et al. 2018).

130 The study by Marvasi et al. (2009) has shown that the bacterial colonization of medieval
 131 stained glass windows in Florence cathedral was favored by dust, crusts and organic matter. The
 132 inside of the windows did not exhibit any visible damage, whereas the outside of the glass was clearly
 133 contaminated with crusts, except for the green parts of the windows where no damage was detected,
 134 even on the external parts. Hence, the authors analyzed the chemical composition of the green glass,
 135 hypothesizing an antibacterial activity of the glass component(s). Copper (present in high quantities
 136 in green glass), which in its Cu²⁺ form is toxic for microbial cells, and has been demonstrated to
 137 reduce colonizer biodiversity (Milanesi et al. 2006), was not the cause of the lower number of
 138 microorganisms that were found, since most of the bacteria were resistant to CuSO₄. Similarly, lead
 139 (Pb) was not involved, since it was only present on the internal side of the glass. However, a higher
 140 Na content was found in the green glass than in the other colored glass. The Na-rich glass also
 141 displayed a higher silica content (around 65%) than the K-rich glass. In particular, the green glass
 142 was found to be of the so-called Na-rich alkaline silicate-sodium type of glass that is typical of the
 143 medieval Renaissance period. This condition is unfavorable for microbial growth. Conversely, the K-
 144 Ca-SO₄ crusts found on the other colored glass (ascribable to gypsum and syngenite, as determined
 145 by means of Fourier Transform Infrared Spectroscopy, FTIR) created a microenvironment that was
 146 able to retain nutrients, microorganism and moisture, which in turn protected the bacteria from the
 147 high temperatures reached as a result of exposure to sunlight during the day. The combination of
 148 microscopic/biochemical identification with 16S rDNA-based molecular tools indicated that the
 149 populations found inside the cathedral were different from those found on the outside glass;
 150 *Firmicutes* in particular were absent on the inside windows. The clean glass (inside and green) mainly
 151 hosted *Actinobacteria* and *Proteobacteria*. The former were previously also found on other Cathedral
 152 windows (Krumbein et al. 1991; Rölleke et al. 1999), whereas the proteobacteria *Brevundimonas* are
 153 typical of alkaline and nutrient-poor environments (Abraham et al. 1999). A high number of spore-
 154 forming *Bacillus* and *Paenibacillus* were found in the crusts, thus indicating that the sporulation
 155 ability could have been responsible for their resistance and long survival ability, as reported above.

Wood and paper biodeterioration: the role of lignocellulolytic microorganisms

Lignocellulosic material is the main component of paper, vegetal textiles and wood. Lignocellulose mainly includes cellulose, hemicellulose and lignin, whose relative amounts may widely vary depending on the specific item (Bomble et al. 2017). It is an energy/carbon substrate for many different microorganisms, including both bacteria and fungi. These organisms may damage library book collections, ancient documents, drawings and photographs (Cappitelli et al. 2010), as well as wooden objects, e.g. ancient coffins, weapons, Native American houses, boats, bridges, ships and shipwrecks (Björdal 2012a and 2012b; Björdal et al. 1999; Palla et al. 2013; Singh 2012). Lignocellulose deconstruction in the biosphere is a complex phenomenon which is generally catalyzed by mixed microbial communities, in which each strain provides its peculiar enzyme activity(ies) (e.g. lignin and/or cellulose and/or hemicellulose depolymerizing action) (Bomble et al. 2017). The best characterized lignin degraders are white-rot and brown-rot fungi which use oxidative mechanisms, i.e. peroxidases and laccases or Fenton chemistry, respectively (Bomble et al. 2017). Hemi-/cellulolytic microorganisms mainly biosynthesize glycoside hydrolases and polysaccharide lyases, although other biochemical mechanisms for hemi/cellulose depolymerization have been recently discovered (Bomble et al. 2017). Cellulolytic organisms are also involved in the deterioration of fabric of vegetal origin. However, this aspect will be treated in more detail in the next section (textile deterioration).

Wood

Unlike what occurs for above-ground wood, whose decay is mainly due to strictly aerobic fungi (e.g. Basidiomycetes, such as white-rot and brown-rot fungi) and is very fast (less than one year- a few years) (Daniel and Nilsson 1997), buried or waterlogged wood is prevalently degraded by moderate aerobic and anaerobic organisms (soft rot Ascomycetes and Deuteromycetes, tunneling bacteria and erosion bacteria) (Singh 2012). In the latter case, the degradation occurs at a much lower rate (hundreds, sometimes thousand of years) (Björdal 2012a). Lignocellulose degradation is much faster on land (provided that wood is in contact with the ground) than in aquatic environments, because of the greater oxygen availability, which also accounts for lignin degradation. In underwater sites, such as peatlands, seas and lakes, only water-dissolved oxygen is available, thus microaerophilic and anaerobic organisms prevail. Since their metabolism is slower, decay takes longer. It is for this reason that important archeological wood samples, especially ships, have been preserved until now. For example, the Vasa warship and the Oseberg Viking ship (Fig. 1) have both been preserved by an aquatic environment in which a “low profile degradation” occurs (Björdal 2012a). However, in spite of the apparent good state of preservation (physical integrity, presence of colors, ornaments etc.)

189 archeological wood behaves very differently from recent sound wood: it is spongy and very soft, and
 190 if it is not kept wet, it will crack and disintegrate (Björdal 2012a).

191 The first attempt to identify microbial communities on waterlogged archeological wood was
 192 reported by Björdal and co-workers in 1999. These authors demonstrated, by means of SEM, that
 193 anoxic-tolerant erosion bacteria (EB) can be found throughout wood tissue, whereas a prevalence of
 194 tunneling bacteria (TB) and soft root fungi (SR, Ascomycetes) can be observed in the outer layers.
 195 EB attack was also monitored by means of polarization light microscopy and transmission electron
 196 microscopy (TEM), and the results demonstrated cellulose depletion and lignified cell-walls with
 197 typical crescent-shaped grooves (Singh 2012). Although the authors did not identify the bacteria,
 198 these studies had the merit of demonstrating that biological deterioration was the main reason for
 199 wood damage in this extreme environment. The environment was in fact slightly alkaline, and the
 200 presence of bacteria was determined microscopically. Furthermore, these authors attempted to
 201 establish the location of the ship waterline (by means of microscopic observations), which could
 202 constitute an important parameter to help estimate the ship weight and hence the type of material
 203 transported. The study compared the microbial populations of two waterlogged archeological ships.
 204 In the former, found in the site named Kronholmen (Sweden), the typical decay of EB was observed,
 205 thus suggesting a very early sinking of the ship, which favored anaerobic degradation. On the other
 206 hand, an abundance of SR fungi attack was reported for the latter ship found in Kraveln (Sweden),
 207 thus indicating that the decay probably occurred when the ship was still sailing. Finally, a medieval
 208 house found in the terrestrial medieval layers of the Vadstena site (Sweden) displayed the particular
 209 signature of brown rot fungi degradation (Björdal et al. 1999). Since these organisms are even more
 210 aerobic than SR, this finding suggests that the house was colonized by decay-microorganisms when
 211 it was still in use. These studies have all had a great significance for archeologists.

212 It should be underlined that, apart from oxygen (lower oxygen, lower decay), other factors
 213 (such as soil type, salinity, pH and temperature) also account for a faster or slower degradation, and
 214 favor certain microbial populations (Björdal 2012a). For instance, salty waters favor wood
 215 degradation by marine borers even earlier than microbial intervention. High nitrogen availability
 216 favors SR fungi, while EB seem more adapted to low nitrogen concentrations (lower than 0.1%) and
 217 TB are selected in a relative alkaline environment (Björdal 2012b). Finally, the susceptibility of each
 218 type of wood is crucial as is the wood species. In general, type1 SR prevalently colonize
 219 gymnosperms, whereas type 2 SR colonize angiosperms (Singh 2012). Moreover, oak and pine
 220 display a higher resistance to decay than birch (Björdal 2012a).

221 In 2004, Helms and coworkers analyzed anaerobic bacteria that colonized an ancient wooden
 222 spear shaft, which was found in an archaeological site in southern Jutland (Denmark), by extracting

223 and amplifying 16S rDNA sequences from the individual cultures after growth on glucose and xylose
 224 at 14°C and 20 °C, and they found clones belonging to alpha, beta and delta proteobacteria. Nilsson
 225 et al. (2008) have recently characterized the microbial populations of EB on archeological
 226 waterlogged wood using DNA-based techniques, while referring to the ribosomal RNA clone libraries
 227 and DGGE set up by Landy et al. (2008). Although most of the bacteria belonged to the *Cytophaga*-
 228 *Flavobacteria* cluster, the identification of these bacteria at a species level has still not been achieved.
 229 A review article that reported on the biodegradation phenomena that occurs on underwater wrecks in
 230 the Baltic Sea (Björdal 2012b) describes how true wood degraders (e.g. microorganisms that are able
 231 to directly depolymerize lignin and/or cellulose and/or hemicellulose) generally coexist with bacteria
 232 (which are also responsible for iron and sulfur cycling) that are able to use the soluble sugars, such
 233 as mono- and oligo-saccharides, or end-products (e.g. lactic acid, acetic acid, ethanol) derived from
 234 lignocellulolytic species metabolism. This points out the important synergistic interactions that occur
 235 among different underwater wood inhabitants.

236 A combined approach (SEM, bacterial cultures and DNA-based techniques) was used by Palla
 237 et al. (2013) to characterize the bacterial population of an underwater fleet wreck (36 B.C.) in the
 238 Sicilian area. Amplification of specific ribosomal DNA sequences, like the Internal Transcribed
 239 Spacer (ITS), allowed *Xanthomonas*, *Pseudomonas*, *Sphingomonas* and *Marinobacter spp* to be
 240 identified.

241 Paper

242 As far as paper documents are concerned, the work by Cappitelli et al. (2010) led to the
 243 identification of cellulolytic microorganisms on an ancient Italian manuscript (dating back to 1293
 244 A.D.) as well as on the Leonardo da Vinci Atlantic Code (early years of 1500 A.D.). For the latter,
 245 the authors developed a non-invasive sampling procedure with sterile nitrocellulose membrane filters
 246 and used them for direct DNA extraction. This DNA was studied by means of Denaturing Gradient
 247 Gel Electrophoresis (DGGE) (Fig. 2a) of the 16S rRNA and ITS regions, and this allowed band
 248 patterns to be analyzed by the principal component analysis (PCA) multivariate technique. The
 249 construction of bacterial and fungal clone libraries is useful in the detection of true degraders among
 250 different organisms (for instance, skin microbiota contaminants, insect-carried bacteria) and to reveal
 251 the microorganisms that possess the endo- or exo-glucanases that are able to depolymerize cellulose.
 252 Cellulolytic activities can also be detected using cellulose powder mixed in an agar medium and then
 253 observing whether a clear halo appears in the agar plate (Cappitelli et al. 2010). Electronic nose
 254 technology can also help in discriminating volatile acids produced by the cellulolytic activities of
 255 *Aspergillus* and *Eurotium* (Canhoto et al. 2004).

In short, the analyses of ancient paper have highlighted that microbial colonization occurs mainly when the relative humidity is above 65% and the temperature is higher than 23°C, as this facilitates the growth of several fungal genera (*Alternaria*, *Aspergillus*, *Mucor*, *Penicillium*, *Rhizopus*, *Cladosporium*, *Chrisosporium* and *Trichoderma*) as well as cellulolytic bacteria. It should be pointed out that modern paper is different from ancient paper: in the former, apart from cellulose, other components of wood pulp, such as hemicellulose, pectin and lignin, can represent a suitable carbon substrate for microbial colonization. Furthermore, modern paper documents are treated with gelatin and pigments to confer additional properties, thus constituting a supplementary source of nutrients for microbial colonization (Cappitelli et al. 2010).

Textile material biodeterioration: cellulolytic, keratinolytic and esterase-producing microorganisms.

Archeological fabrics (Native Indian clothes, Pre-Columbian and Egyptian textiles, soldiers' uniforms, ecclesiastical vestments, shrouds, carpets, tapestries, oil-on-cotton paintings) are precious items that generally reveal a poor conservation quality. Microbial growth on textiles can produce unwanted pigmentation (e.g. blue or brown spots) discoloration, the presence of biofilms, but also the loss of strength, a decrease in elasticity, depolymerization, disruption of the fiber structure with textile cracking and fragmentation, all of which creates damage that needs to be repaired, and the presence of the microorganisms that are responsible has to be ascertained.

Textiles constitute a nutrient rich environment that can support the growth of both bacteria and fungi. Clothes such as nurses' uniforms can even act as a reservoir for multidrug resistant bacteria (Neely and Maley 2000). The intrinsic nature of a textile is crucial in favoring or preventing colonization. Because of their hydrophilic structure, natural fabrics retain humidity and thus provide a perfect habitat for microbial colonization. On the other hand, synthetic hydrophobic fibers are more recalcitrant to biodegradation. External factors, such as high relative humidity, light exposure, high temperature, spontaneous oxidation and aging, can also be responsible for inducing a faster degradation (Szostak-Kotowa 2004). However, degradation is just as likely in dark sites, such as tombs, graves and crypts, because of the high water content (Gutarowska et al. 2017).

As far as pigmentation is concerned, tents, sails and beach umbrellas, being exposed to sunlight and humidity, can support the growth of algae that generate green pigments, whereas raw wool (fleece) can be colonized by *Pseudomonas aeruginosa*, which generates both green (in an alkaline environment) and red (in acidic conditions) pigments during wool degradation. Yellow, orange, brown or black pigments can also be synthesized by *Brevibacterium*, *Bacillus*, *Rhodococcus*, *Corynebacterium*, *Achromobacter*, *Streptomyces*, and by fungi such as *Rhodotorula*, *Penicillium*, *Aspergillus*, *Cryptococcus* (Gutarowska et al. 2017). Discoloration is often the consequence of an

altered pH, due to microbial metabolism. Culturing is not a suitable method for detecting the “guilty microbes” since about 99% of microbial strains are viable and metabolically active, but not culturable. Hence, culture-independent methods can be applied successfully to solve the problem. Techniques based on the amplification of target/marker genes (e.g. 16S rRNA in bacteria and 18S rRNA in fungi), followed by different approaches, such as DGGE, ARDRA (Amplified Ribosomal DNA Restriction Analysis), SSCP (Single strand conformation polymorphism), ARISA (Automated method of ribosomal intergenic spacer analysis) and NGS (Next Generation Sequencing), have been used to characterize microbial populations at the species level (Lech et al. 2015). However, culturing methods followed by molecular-based microbial identification have recently also been used by Pietrzak and co-workers (2017) to identify microbial populations on Pre-Columbian Textiles made of cotton and lama- or alpaca-wool. Bacteria from the *Bacillus*, *Oceanobacillus*, *Staphylococcus*, *Micrococcus*, *Pseudomonas* genera strains were isolated as well as more abundant quantities of *Kokuria rosea* and *Paracoccus yeei*. The most common fungal genera were *Aspergillus*, *Penicillium* and *Cladosporium*. The authors underlined that a greater biodiversity can be present on cotton samples, with 11 different species having been isolated (Pietrzak et al. 2017).

Vegetal and animal fibers display different resistance to biodegradation (the former being more sensitive than the latter), and they hence have different destinies: some microbial degradative pathways will be described in the following sections. However, it should be pointed out that susceptibility to biodeterioration is also related to the type of weave, the textile thickness and the polymerization extent of the fiber, as well as to its amorphous or crystalline state.

Cotton, linen, jute and hemp

Plant-derived fabrics are susceptible to the action of lignocellulolytic enzymes. Non-cellulosic components, like lignin, render the fiber more resistant to degradation: for example, hemp and jute, which contain a high percentage of lignin, degrade more slowly than cotton, which lacks such compounds (Gutarowska et al. 2017). Conversely, pectin and hemicellulose are easily degradable and favor microbial colonization, which in turn promotes the attack of cellulolytic organisms (Szostak-Kotowa 2004). Three types of hydrolytic enzymes are required for complete conversion of cellulose into glucose (the true energy-generating carbon substrate): 1) *exoglucanases*, which cleave cellulose chains, starting from the reducing or non-reducing end, and generate cellobiose or glucose 2) *endoglucanases*, which cleave internal glycosidic bonds of amorphous cellulose in a random manner and generate different-length oligosaccharides 3) *beta-glucosidases*, which convert short oligosaccharides, such as cellotriose and cellobiose, to glucose. Generally, bacteria such as *Cellulomonas*, *Cellvibrio*, *Clostridium*, *Cytophaga*, *Bacillus*, *Arthrobacter*, *Sporocytophaga*, *Microbispora*, *Pseudomonas*, *Nocardia* and *Streptomyces* act from the fiber surface toward the

interior. Conversely, most fungi (*Aspergillus*, *Verticillium*, *Penicillium*, *Mucor*, *Myrothecium*, *Thricoderma*, *Rhizopus*, *Alternaria*, *Fusarium*, *Aureobasidium* and *Cladosporium*), or their spores, penetrate directly into the fiber lumen, where they generate a mycelium that is responsible for the secretion of extracellular cellulolytic enzymes (Szostak-Kotowa 2004). The final effect of cellulase action is the depolymerization of cellulose, which leads to an impaired fiber strength.

Wool and silk

Animal-derived fabrics are a little more resistant to degradation. Their main components are proteins: keratin in wool and fibroin and sericin in silk, hence, proteases are required for degradation.

Keratin is a compact structure made up of parallel or antiparallel peptide chains, cross-linked by disulfide bridges. This is why hair and wool are long lasting post-mortem. However, insects can attack wool keratins, as well as bacteria and fungi. Keratinolytic bacteria (*Alcaligenes*, *Bacillus*, *Proteus*, *Pseudomonas* and *Streptomyces*) are less efficient than fungi. Among the latter, *Fusarium*, *Rhizopus*, *Aspergillus*, *Penicillium*, *Microsporum*, *Chaetomium*, *Trichophyton* and *Trichoderma* have been described as significant keratin degraders. The degradative action begins with a reduction of the disulfide bridges, which results in a weaker polypeptide chain that is suitable for proteolytic attack (Szostak-Kotowa 2004). Peptide degradation can also give rise to ammonia as a result of amino acid deamination (Gutarowska et al. 2017).

As far as silk is concerned, its main protein fibroin is made up of fibers held together by sericin, a second protein that acts as an adhesive. While fibroin is essentially constituted (more than 90%) by four amino acid repeats (glycine, alanine, serine and tyrosine) that are less attractive as microbial food, sericin is the first one to be utilized as a nutrient by microorganisms. Degummed (i.e. sericin-deprived) silk is degraded at a slower rate, and two months are required before a decrease in strength can be detected. Nevertheless, sericin-deprived silk is more susceptible to light damage. Although only *Pseudomonas cepacia* can use fibroin as a carbon source, *Bacillus*, *Serratia*, *Pseudomonas* and *Streptomyces* have also been found in a degradation mixture, thus suggesting the occurrence of co-metabolization (Forlani et al. 2000; Seves et al. 1998). One fungal strain of *Aspergillus niger* has also been described as being able to modify the fibroin structure (Szostak-Kotowa 2004).

Man-made textiles

Man-made textiles may be of natural or synthetic origin. Viscose (also called rayon), a natural fiber originating from cellulose, is very sensitive to microbial degradation. Other synthetic polymers, as previously mentioned, display a certain degree of resistance, because of their hydrophobicity, but also because of their intrinsic chemical bonds (i.e. ether), which are unusual in natural compounds. Polyurethanes are not so hydrophobic, and they can therefore bind water, thus favoring microbial

colonization. Polyester-containing polyurethanes are generally degraded faster than polyether-containing polyurethanes, thus confirming the importance of the intrinsic chemical bonds (Seal 1988). Polyurethane is the most suitable polymer for microbial degradation, because it contains domains (ester bonds, urea) that mimic natural bonds. Extracellular fungal esterases may catalyze polyurethane degradation: *Alternaria*, *Aspergillus*, *Penicillium*, *Trochoderma* and *Cladosporium* are among the fungal genera involved in this process. Polyurethane is often employed for the production of bathing wear, because of its elasticity and flexibility. Swimsuits from Olympic winners in museums are at risk of damage as a result of exposure, and particular care should be taken to house these items in a sterile environment (Rowe and Howard 2002).

Regardless of their intrinsic features (lesser or higher degradability), synthetic fabrics are often treated with oils, fats, pigments and plasticizers to finish the textile. These additives can contain nutrients that support microbial growth, and later favor fiber disruption and fabric deterioration. A paradigmatic example is polyvinyl chloride (PVC), which is used for waterproof coatings, and which is not a microbial nutrient in itself, but is often treated with plasticizers, such as aliphatic polyesters, to enhance elasticity. Aliphatic polyesters and lactic acid polymers (such as PLA) are easily degraded by microorganisms that can later alter PVC by co-metabolism (Webb et al. 2000). Furthermore, during use, dirty particles can accumulate, thus adding supplementary nutrients for colonization.

Polypropylene and polyamide fibers, like nylon, are generally degraded after exposure to light, since UV-induced photo-degradation accelerates the bioavailability of shorter chain polymers. Among the bacteria, *Bacillus*, *Bravibacterium*, *Achromobacter* and *Protaminobacter* can all degrade nylon after exposure to light. This should be taken into account when synthetic materials of cultural heritage interest are on display in museum areas under intense light. On the other hand, a *Pseudomonas aeruginosa* strain that is able to hydrolyze nylon without prior light exposure has been observed (Priyambada et al. 1995). As far as polyacrylonitrile (acrylic textiles) is concerned, an *Arthrobacter* strain, which can utilize acrylonitrile as a nutrient, has been isolated, but not its polymer (Seal 1988). Polyethylene terephthalate (PET), like other aromatic polyesters, seems to be, among plastic polymers, the most resistant to microbial attack (Szostak-Kotowa 2004). However, due to the intense search of xenobiotic-degrading organisms, a Gram-negative aerobic beta-proteobacterium, named *Ideonella sakaiensis*, which is able to degrade PET, was isolated two years ago (Yoshida et al. 2016). Although some constraints limit full degradation (i.e. the process is relatively slow, access to the PET polymer fibers in the smooth plastic surface is not so easy), there is good possibility that this, and possibly other bacteria, will be able to attack PET objects in the future.

Bone deterioration: contribution of collagenase and amino acid racemization activities.

391 Among the various animal tissues, bones are the best preserved after death. It is for this reason
 392 that archeological bones are so important in the reconstruction of events, such as the historical life-
 393 period of a civilization found in an excavation site, the species determination of bones of unknown
 394 taxonomy and the cause and the age of death of human remains. However, deterioration can also
 395 occur on bones, and microbial degradation plays a crucial role. This event occurs very early (3
 396 months-5 years after death), depending on the humidity, temperature and the oxygen availability, and
 397 is largely determined by endogenous gut bacteria or soil microorganisms (Jans et al. 2004). The
 398 macroscopic alteration of bones is named “tunneling”, since empty tunnels of about 10 μm of
 399 diameter appear, thus indicating that both the mineral and the proteinaceous components of the bones
 400 have been destroyed by microorganisms. A high percentage of tunneling is due to bacterial activity
 401 (Jans et al. 2004). Bacterial degradation generally occurs on demineralized bones, since both body
 402 fluids and soil components can create an acidic environment that favors demineralization. However,
 403 some bacteria can directly liberate proteins from inorganic material (Child 1995a; Kendall et al.
 404 2018).

405 Collagen is the most represented protein in bones. Although the terminal parts of collagen are
 406 sensitive to the proteolytic action of chymotrypsin and pepsin, the helical portion of collagen is only
 407 hydrolyzed by specific collagenases, i.e. enzyme complexes made up of six different subunits
 408 containing zinc in the catalytic center. Because of this resistance to enzymatic degradation, collagen
 409 is a long-lasting protein (Giuffrida et al. 2018). However, the typical bacterial collagenases of
 410 anaerobic Clostridia (for instance, *Clostridium histolyticum*), but also of aerobic *Mycobacterium*
 411 *tuberculosis* (Child 1995b), *Pseudomonas spp*, *Aeromonas* and *Klebsiella* (Child et al. 1993) can alter
 412 collagen stability. Unlike what is observed in bacteria, only one fungal species (*Chrysosporium spp.*),
 413 among those isolated from bones, displays collagenase activity, thus suggesting that soil fungi are not
 414 the first bone colonizers (Child et al. 1993).

415 The extent of racemization of bone collagen was used in the past to determine the time that
 416 had elapsed since the death of an individual, or to predict the preservation of DNA in the bone (Bada
 417 and Protsch 1973; Poinar et al. 1996), but both uses have been abandoned, since the open-system
 418 nature of bone and the structure of collagen itself prevent predictable patterns of diagenesis (Collins
 419 et al. 2009; Demarchi and Collins 2014; Wadsworth et al. 2017). Unfortunately, some bacteria
 420 (*Pseudomonas spp*, *Aeromonas*) can express non-specific amino acid racemases that can alter the
 421 ratio between R and S forms, as well as preferentially metabolize one enantiomeric form (Child et al.
 422 1993), thus making the real age at death of archeological bones questionable. Jans and co-workers
 423 (2004) combined histology and mercury intrusion porosimetry to study archeological bones from
 424 excavations in different geographical areas (Mediterranean, coastal, subarctic and continental). They

demonstrated that bones from the abdominal area are rapidly colonized by intestinal bacteria, such as *Clostridia*, *Staphylococci* and *E. coli*, whereas dismembered animal bones are not attacked by endogenous microflora and therefore constitute a nutrient-rich medium for soil fungi. Since most fungi are strictly aerobic, oxygen availability is a limiting factor for degradation. Therefore, a better conservation state can be observed when the burial ground has a low redox potential.

Painting biodeteriogens: lipolytic, amylolytic, proteolytic, solventogenic, acidogenic and pigment-producing microorganisms.

Wall and easel paintings can suffer from biodeterioration related to the degradation of the material itself (due to microbial enzymatic activities), or to the production of primary or secondary metabolites. Metabolic end-products, such as surfactants, solvents and acids, can cause the discoloration or corrosion of artefacts. Secondary metabolites, like pigments (generally produced as defense molecules), can produce stains. Since a painting can be performed on any material, the number of possible nutrients for microbial growth increases. Several layers should be considered, e.g. a support material, thickeners and glues, pigments, emulsifiers, protective films, but also unwanted exogenous particles that can carry nutrients.

Carbon sources found in wall paintings can select autotrophic bacteria, whereas easel paintings (on wood, wool, silk, paper, etc.) support the growth of heterotrophic organisms. A nitrogen source is sometimes present in the support (keratin in wool, fibroin in silk), or can be supplied by the glues (for instance, collagen-based glues) or the emulsifiers/protectants (milk was frequently used, before the acrylic era, to create a protective glossy film on paintings, thus supplying caseins). However, natural pigments (e.g. those based on egg-yolk) are the best sources of different nutrients, especially on ancient medieval paintings (Giuffrida et al. 2018). Egg-white and egg-yolk can both contribute to albumin and vitellogenin availability for microorganisms, but can also supply lipids as an energy source. In general, it is possible to state that wall paintings are more susceptible to biodeterioration than easel paintings, since they are generally conserved in rain-exposed environments or in humidity rich hypogeal sites that favor microbial colonization. For this reason, most literature data refer to frescoes.

Several alternative approaches have been employed/developed to characterize the causative agents of biodeterioration. In 1996, Rölleke and co-workers characterized the microbial population on a 13th century wall painting belonging to the Chapel of the Herberstein Castle in Austria. By means of electron microscopy, they detected bacteria that had a filamentous morphology. Culturing allowed the growth of only five strains, three of which gave rise to pigmented colonies (white, yellow and red, respectively). DGGE analysis on the amplified DNA from the purified isolates revealed the presence of *Actinomycetales* (high G+C content Gram-positive bacteria like *Arthrobacter*, *Pseudonocardia*

459 *and Streptomyces*) and *Acinetobacter lwoffii*. The former possess the ability to form hyphae that can
 460 cause frescoes to lose their integrity through a mechanical disruption of the wall layers. The latter can
 461 occur since many species of the same genus (Gram-negative belonging to the gamma proteobacteria)
 462 use short-chain fatty acids and lipids as preferential carbon sources (Violetta et al. 2014). It was
 463 probably at the expense of egg-yolk pigments or oils used as emulsifiers that these bacteria could
 464 grow on the Chapel of the Herberstein Castle paintings. The DGGE approach was also used to study
 465 DNA aliquots, sampled directly on the wall painting, without prior cultivation. *Halomonas*,
 466 *Clostridium* and *Frankia* were detected. *Frankia*, an Actinomycetes that displays very slow growth,
 467 can be responsible for mechanical damage due to hyphae, although it is seldom referred to in the
 468 literature because it is difficult to cultivate. *Halomonas* (Gram-negative belonging to the gamma
 469 proteobacteria) can be found in extremely salty environments (e.g. the salt efflorescence areas of
 470 frescos) and can cause biodegradation, due to acid production, when its metabolism shifts from
 471 aerobiosis (respiration) to anaerobiosis (fermentation). *Clostridium* (low-G+C content Gram-positive
 472 bacteria) are obligate anaerobes that produce acids and alcohols from both carbohydrate and protein
 473 fermentation. Some alcohols, like ethanol and butanol, can have a solvent action on pigments, thus
 474 causing fresco discoloration. Finally, the authors highlighted the importance of using molecular
 475 methods to ensure the right ratio among the different populations. For instance, although
 476 *Acinetobacter* gives rise to a significant biomass, it was not so abundantly represented in the DGGE
 477 pattern (Rölleke et al. 1996). On the other hand, the same work group found different microorganisms
 478 using cultivation vs molecular methods, and suggested that it is necessary to combine the two
 479 techniques in order to have a true picture of what happens on a mural painting surface (Gurtner et al.
 480 2000).

481 Radaelli and co-workers (2004) characterized the microbial populations present on a damaged
 482 17th century fresco in Assisi (Italy) through morphological observation and traditional biochemical
 483 methods. They found a prevalence of Gram-positive cocci (mainly *Micrococcus* and *Staphylococcus*),
 484 followed by Gram-negative rods (mainly *Pseudomonas* and *Alcaligenes*) and then by Gram-positive
 485 rods (only *Corynebacterium* and *Bacillus*). The most abundant species, *Staphylococcus cohnii* and
 486 *Bacillus licheniformis*, were submitted to molecular bio-typing to detect whether there were any intra-
 487 species differences among the several strains that had been isolated. Restriction Fragment Length
 488 Polymorphism (RFLP) (Fig. 2b) and Random Amplified Polymorphic DNA (RAPD) analyses both
 489 revealed a genetic similarity of the studied strains. Considering the biodeteriogenic potential of the
 490 different isolates, the authors proved that *Pseudomonas maltophilia* was absent in the less damaged
 491 areas, thus suggesting its role in the degradation of the most damaged parts (Radaelli et al. 2004).

Fatty acid methyl ester analysis (FAME) (Fig. 2c) was used to detect the biodiversity of bacterial strains isolated from a wall painting belonging to St Catherine's Chapel (Herbstein, Austria) and to St. Martin's Church (Greene, Germany) (Heyrman et al. 1999). Again in this case, Gram-positive bacteria, including *Bacillus*, *Paenibacillus*, *Arthrobacter*, *Micrococcus* and *Staphylococcus spp.* were ubiquitous and highly represented. *Nocardioform actinomycetes* were only found in the Greene site, whereas *Halomonas* was only found in the Herbstein site, suggesting that particular conditions favor the presence and selection of these species. The authors explained that the high number of *Bacillus* strains they found in samples from different geographic sites was due to the fact that the sporulation ability makes them able to survive for long periods of time.

An interesting paper by Imperi et al. (2007) reported the characterization of both bacteria and pigments detected on a 9th century fresco, illustrating scenes from the Genesis (Fig. 3). These byzantine paintings, discovered in 1963 in the Crypt of the Original Sin near Matera (Italy), had suffered from water infiltration, carbonate precipitation and discoloration. Former attempts to characterize the microflora, by means of morphological and culture-based methods, had revealed the presence of cyanobacteria and green algae. Later, an unwanted reddish pigmentation that covered much of the painted area appeared. Background-subtracted *in situ* micro Raman spectra of the pigmented area revealed three major bands, ascribable to the vibrational mode of the C-CH₃ groups, to the single C-C bonds and the double C=C bonds, respectively. The analytical results made it possible to conclude that the pigments were carotenoid molecules. Both ARDRA and DGGE were used for microbial typing. Actinobacteria (in particular *Rubrobacter radiotolerans*), α -Proteobacteria (in particular *Erythrobacter spp.*), Bacteroidetes (in particular *Sphingobacterium*) and Cyanobacteria were found to be present, as well as Archea such as *Halococcus* and *Haloferax*. However, Archea only represented a numerically insignificant contaminant (less than 0.1% of the 16S rRNA gene pool), whereas *Rubrobacter radiotolerans* was abundant (about 87% of the 16S rRNA gene pool per sampled site) in almost all the samples from the pigmented area. In order to better assess the cause of the pigmentation, pigments produced by *Rubrobacter radiotolerans* were analyzed by micro Raman spectroscopy, and it was demonstrated that they were the same as the pigmented area on the fresco. These carotenoids, named bacterioruberins, have a C-50 length and display 13 conjugated double bonds. However, this result cannot exclude that other microbial strains (eubacteria, such as *Micrococcus* and *Arthrobacter* and archea like *Halococcus* and *Haloferax*) could also synthesize ruberins, since the Raman analysis was unable to distinguish bacterioruberins from different species.

Motion picture films and photographic material biodeterioration: the contribution of gelatine liquefiers.

525 Cinematographic films and photographs have an important historical value. They are both
 526 composed of three basic elements, namely a *support*, an *image-forming layer* and a *binder* for the
 527 image-forming emulsion. These layers can undergo both abiotic deterioration and microbial attack.
 528 The latter can cause degradation, pigmentation and discoloration (Abrusci et al. 2005). Owing to their
 529 relative recent origin, no attention has been paid to ensuring their conservation, and it is only in the
 530 last two decades that papers dealing with this problem have begun to appear in the literature.

531 Until the end of the last century, the support material was made of cellulose esters, mainly
 532 cellulose nitrate (used since the end of the 19th century until 1950) and cellulose triacetate (CTA, in
 533 use between 1950 and 2000). Both are excellent growth media for cellulolytic bacteria and fungi,
 534 although the higher the esterification is, the higher the resistance to microbial degradation (Sakai et
 535 al. 1996). Since 1990, synthetic plastics, such as PET (polyethylene terephthalate), have been used to
 536 overcome the poor chemical stability of natural polymers, and these are able to guarantee a 10 times
 537 longer life-time than cellulose esters. However, microorganisms that are able to degrade PET are
 538 being described more and more frequently in the literature, and *Ideonella sakaiensis* 201-F6 has
 539 recently been included in this list (see the previous section) (Yoshida et al. 2016).

540 As regards support material, before undergoing cellulolytic degradation by fungi and bacteria,
 541 CTA must be de-acetylated by esterases. De-acetylation can be also obtained abiotically under
 542 suitable temperature and moisture conditions (the phenomenon that releases acetate has a
 543 characteristic odor which is referred to as a “vinegar smell”) (Abrusci et al. 2004a). When a suitable
 544 degree of de-acetylation has been obtained, and at least two adjacent glucose units are available,
 545 cellulase-mediated catalysis can occur. *Aspergillus*, *Penicillium*, *Fusarium* and *Trichoderma* have
 546 been reported as CTA degraders among fungi, while *Pseudomonas* and *Neisseria* have been reported
 547 among bacteria (Abrusci et al. 2004a).

548 Photosensitive emulsion includes silver salts (in black and white photographs) and pigments
 549 (in colored photographs) mixed with gelatin (an amorphous transparent material that forms a gel
 550 network, obtained by thermal denaturation of animal collagen), which constitutes the binder (Fig. 4).
 551 Although silver can be toxic for living organisms, most fungi display the ability to reduce dangerous
 552 oxidized silver ions into metallic silver, which is then accumulated as nanoparticles on the cell-wall
 553 surface (Sclocchi et al. 2013). However, the deterioration of films is very seldomly linked to the
 554 microbial utilization of metals and pigments.

555 On the contrary, gelatin is an excellent growth substrate for several bacterial genera (*Bacillus*,
 556 *Clostridium*, *Micrococcus*, *Staphylococcus*, *Streptococcus*, *Enterococcus* *Pseudomonas*, *Aeromonas*,
 557 *Serratia*, *Burkholderia*, *Yersinia* and *Salmonella*), which are named “gelatin liquefiers”. De Clerck
 558 and De Vos (2002) reported gelatin contamination by endospore-forming aerobic *Bacillus* spp. Such

long-term survivors can constitute a risk for photographic material. Abrusci and co-workers (2005) characterized the microbial populations of black and white motion picture films belonging to the Spanish cinematography Archives by combining morphological, biochemical and molecular-based methods. These authors found that all the isolated fungi (*Aspergillus*, *Penicillium*, *Trichoderma*, *Cladosporium*, *Mucor*, *Alternaria*, *Phoma* and *Cryptococcus*) were able to degrade gelatin, whereas only 7 bacterial strains (belonging to the *Bacillus* and *Staphylococcus* genera), out of a total of 14 isolated from the film, displayed gelatinase activity. Gelatinase efficiency was established by means of both viscosity decay profiles (Abrusci et al. 2004b and 2007) and chemiluminescence emission (Abrusci et al. 2007).

Borrego et al. (2010) studied the microbial population that colonized the inside of the Photographic Library of the National Archive in Cuba. Samples were collected in the air (by means of a sedimentation method) and on the surface of the photographs (using cotton swabs). All the microbial isolates were tested to establish their cellulolytic, proteolytic and amylolytic activities. They found a prevalence of proteolytic strains in the photographic material. Only one Gram-negative rod (namely *Pseudomonas* spp) was found on the considered samples. On the other hand, the air samples were colonized abundantly by cellulolytic fungi (which were also acid- and pigment-producers).

Bučková and co-workers (2014) used variable pressure scanning electron microscopy (SEM) analyses coupled with PCR DNA amplification and 16S rRNA (for bacteria), or ITS (for fungi), to characterize the microbial populations present in photographs housed in the “Archivio ente EUR” and “Archivio Centrale dello Stato” in Rome. A significant number of fungal genera, among which *Geotrichum*, *Aspergillus*, *Penicillium*, and the unusual *Zygosporium* were found, as well as bacteria (with a predominance of *Pseudomonas*) on documents that had previously been damaged by water. Any attempt to cultivate these strains was unsuccessful. Curiously, both *Geotrichum* and *Pseudomonas* were present in high abundance, thus suggesting that they were selected because of their resistance to silver ions.

Synthetic polymer-based modern artworks and human history proofs: the risk of xenobiotic-degraders.

Plastic objects, which are frequently present in contemporary art collections as important symbols of history, have recently revealed a risk of deterioration that is comparable with or even higher than that of ancient artworks. Apart from photo-degradation and oxidation, biological deterioration also accounts for damage. Pigments and microbial biofilms are often responsible for superficial damage, but the main problem arises when plastic material is used by microorganisms as

a nutrient for growth. The recent environmental emergency situation has prompted the search for biodegradable plastic polymers, together with efforts to select bacteria that are able to hydrolyze recalcitrant xenobiotic molecules (Yoshida et al. 2016). These bacteria, which generally release acids from their oxidative catabolism, can thus also cause the degradation of high-value plastic items (Cappitelli and Sorlini 2008). As mentioned in the section in which textiles are discussed, polyurethane (Rowe and Howard 2002), polyvinylchloride (PVC) (Webb et al. 2000), nylon (Friedrich et al. 2007) and even PET (Yoshida et al. 2016) can undergo bacterial or fungal colonization and degradation by means of peculiar enzymatic activities, such as urease, esterase and manganese peroxidase (Cappitelli and Sorlini 2008). Spacesuits (Fig. 5), compact discs, Barbie dolls and other toys can be colonized by fungi and bacteria (e.g. *Bacillus subtilis* and *Pseudomonas aeruginosa*) that irreversibly destroy the objects (Breuker et al. 2003; Garcia-Guinea et al. 2001; McCain and Mirocha 1994; Webb et al. 2000). Both *Cladosporium* and *Paecilomyces spp* were identified, by means of traditional methods, on astronauts' suits (Breuker et al. 2003), whereas fluorescent *in situ* hybridization was necessary to identify cyanobacteria and archaea in more complex matrices (Cappitelli et al. 2006). However, since microbial colonization is not always associated with a clear biodeterioration, precious information can be obtained by evaluating the material damage using electronic microscopy, viscosity assessment, differential scanning colorimetry and infrared spectroscopy (Cappitelli and Sorlini 2008). All these data suggest that modern specimens, which constitute a feature of a historical period (1950-today), require adequate strategies to contain their deterioration.

CONCLUSIONS

What do an astronaut's spacesuit, a Viking ship, a shroud, a compact disc, a medieval crypt and a cinematographic film have in common? Regardless of their natural or synthetic origin, they all undergo different forms of deterioration, including microbial degradation. This review article has reported the main biochemical activities involved in cultural heritage biodeterioration, highlighting the importance of cellulases, collagenases, gelatinases, esterases and other enzymes as well as the metabolic pathways of microorganisms in this process. In a period in which the attention of researchers is focused on the synthesis of biodegradable polymers, as well as on the selection of xenobiotic degraders, this mini-review underlines the fragility of modern synthetic man-made objects, which risk having a shorter life than 5000 year-old stone monuments. Progress in this research field is an essential requisite for the preservation and restoration of artistic and cultural heritage items for future generations.

COMPLIANCE WITH ETHICAL STANDARDS

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631

632 **REFERENCES**

- 633 Abraham WR, Strömpl C, Meyer H, Lindholm S, Moore ER, Christ R, Tesar M (1999). Phylogeny
 634 and polyphasic taxonomy of *Caulobacter* species. Proposal of *Maricaulis* gen. nov. with *Maricaulis*
 635 *maris* (Poindexter) comb. nov. as the type species, and emended description of the genera
 636 *Brevundimonas* and *Caulobacter*. Int J Syst Evol Microbiol. 49:1053-1073.
- 637 Abrusci C, Allen NS, Del Amo A, Edge M, Martín-González A. (2004a). Biodegradation of motion
 638 picture film stocks. Journal of film preservation 67:37.
- 639 Abrusci C, Marquina D., Santos A., Del Amo A., Corrales T, Catalina F (2007). A
 640 chemiluminescence study on degradation of gelatine: Biodegradation by bacteria and fungi isolated
 641 from cinematographic films. J Photochem Photobiol A Chem 185:188-197.
- 642 Abrusci C., Martín-González A., Del Amo A., Catalina F., Collado J, Platas G (2005). Isolation and
 643 identification of bacteria and fungi from cinematographic films. Int Biodeterior Biodegrad 56:58-68.
- 644 Abrusci C, Martín-González A, Del Amo A, Corrales T, Catalina F (2004b). Biodegradation of type-
 645 B gelatine by bacteria isolated from cinematographic films. A viscometric study. Polym Degrad Stab
 646 86:283-291.
- 647 Bada JL, Protsch R (1973). Racemization reaction of aspartic acid and its use in dating fossil bones.
 648 Proc Natl Acad Sci 70:1331–1334.
- 649 Beech IB, Sunner J (2004). Biocorrosion: towards understanding interactions between biofilms and
 650 metals. Curr Opin Biotechnol 15:181-186.
- 651 Bellezza S, Paradossi G, De Philippis R, Albertano P (2003). *Leptolyngbya* strains from Roman
 652 hypogea: cytochemical and physicochemical characterization of exopolysaccharides. J Appl Phycol
 653 15:193-200.

- 654 Björdal CG (2012a). Microbial degradation of waterlogged archaeological wood. *J Cult Herit*
655 13:S118-S122.
- 656 Björdal CG (2012b). Evaluation of microbial degradation of shipwrecks in the Baltic Sea. *Int*
657 *Biodeterior Biodegrad* 70:126-140.
- 658 Björdal CG, Nilsson T, Daniel G (1999). Microbial decay of waterlogged archaeological wood found
659 in Sweden applicable to archaeology and conservation. *Int Biodeterior Biodegrad* 43:63-73.
- 660 Bomble YJ, Lin CY, Amore A, Wei H, Holwerda EK, Ciesielski PN, Donohoe BS, Decker SR, Lynd
661 LR, Himmel ME (2017). Lignocellulose deconstruction in the biosphere. *Curr Opin Chem Biol*
662 41:61-70.
- 663 Borrego S, Guimet P, de Saravia S G, Batistini P, Garcia M, Lavin P, Perdomo I (2010). The quality
664 of air at archives and the biodeterioration of photographs. *Int Biodeterior Biodegrad* 4:139-145.
- 665 Breuker M, McNamara C, Young L, Perry T, Young A, Mitchell R (2003). Fungal growth on
666 synthetic cloth from Apollo spacesuits. *Ann Microbiol* 53:47-54.
- 667 Bučková M, Puškárová A, Sclocchi MC, Bicchieri M, Colaizzi P, Pinzari F, Pangallo D (2014). Co-
668 occurrence of bacteria and fungi and spatial partitioning during photographic materials
669 biodeterioration. *Polym Degrad Stab* 108:1-11.
- 670 Canhoto O, Pinzari F, Fanelli C, Magan N (2004). Application of electronic nose technology for the
671 detection of fungal contamination in library paper. *Int Biodeterior Biodegrad* 54:303-309.
- 672 Cappitelli F, Pasquariello G, Tarsitani G, Sorlini C (2010). Scripta manent? Assessing microbial risk
673 to paper heritage. *Trends Microbiol* 18:538-542.
- 674 Cappitelli F, Sorlini C (2008). Microorganisms attack synthetic polymers in items representing our
675 cultural heritage. *Appl Environ Microbiol* 74:564-569.
- 676 Cappitelli F, Principi P, Sorlini C (2006). Biodeterioration of modern materials in contemporary
677 collections: can biotechnology help?. *Trends Biotechnol* 24:350-354.

- 678 Cappitelli F, Principi P, Pedrazzani R, Toniolo L, Sorlini C (2007). Bacterial and fungal deterioration
679 of the Milan Cathedral marble treated with protective synthetic resins. *Sci Total Environ* 385: 172-
680 181.
- 681 Child AM (1995a). Microbial taphonomy of archaeological bone. *Stud Conserv J* 40:19-30.
- 682 Child AM (1995b). Towards and understanding of the microbial decomposition of archaeological
683 bone in the burial environment. *J Archaeol Sci* 22:165-174.
- 684 Child AM, Gillard RD, Pollard AM (1993). Microbially-induced promotion of amino acid
685 racemization in bone: isolation of the microorganisms and the detection of their enzymes. *J Archaeol*
686 *Sci* 20:159-168.
- 687 Collins MJ, Penkman KE, Rohland N, Shapiro B, Dobberstein RC, Ritz-Timme S, Hofreiter M
688 (2009). Is amino acid racemization a useful tool for screening for ancient DNA in bone? *Proc Biol*
689 *Sci* 276:2971-2977.
- 690 Cutler NA, Viles HA, Ahmad S, McCabe S, Smith BJ (2013). Algal 'greening' and the conservation
691 of stone heritage structures. *Sci Total Environ* 442:152-164.
- 692 Daniel G, Nilsson T (1997). Developments in the study of soft rot and bacterial decay. In: Bruce A,
693 Palfreyman JW (eds) *Forest Products Biotechnology*. Taylor and Francis, London, pp 37-62.
- 694 Brown B, Aaron M (2001) The politics of nature. In: Smith J (ed) *The rise of modern genomics*, 3rd
695 edn. Wiley, New York, pp 230-257
- 696 De Clerck E, De Vos P (2002). Study of the bacterial load in a gelatine production process focussed
697 on *Bacillus* and related endospore forming genera. *Syst Appl Microbiol* 25:611-617.
- 698 Del Junco AS, Moreno DA, Ranninger C, Ortega-Calvo JJ, Sáiz-Jiménez C (1992). Microbial
699 induced corrosion of metallic antiquities and works of art: a critical review. *Int Biodeterior Biodegrad*
700 29:367-375.
- 701 Demarchi B., Collins M (2014). Amino Acid Racemization Dating. In: *Encyclopedia of Scientific*
702 *Dating Methods* Springer Netherlands, pp. 1–22.

- 703 Ettenauer JD, Jurado V, Piñar G, Miller AZ, Santner M, Saiz-Jimenez C, Sterflinger K (2014).
 704 Halophilic microorganisms are responsible for the rosy discolouration of saline environments in three
 705 historical buildings with mural paintings. PLoS One 9:e103844.
- 706 Essoussi I, Ghodhbane-Gtari F, Amairi H, Sghaier H, Jaouani A, Brusetti L, Daffonchio D,
 707 Boudabous A, Gtari M (2010) Esterase as an enzymatic signature of Geodermatophilaceae
 708 adaptability to Sahara desert stones and monuments. J Appl Microbiol 108:1723-1732.
- 709 Forlani G, Seves AM, Ciferri O (2000). A bacterial extracellular proteinase degrading silk fibroin.
 710 Int Biodeterior Biodegrad 46:271–275.
- 711 Friedrich J, Zalar P, Mohorčič M, Klun U, Kržan A (2007). Ability of fungi to degrade synthetic
 712 polymer nylon-6. Chemosphere 67:2089-2095.
- 713 Garcia-Guinea J, Cárdenes V, Martínez AT, Martínez M (2001). Fungal bioturbation paths in a
 714 compact disk. Naturwissenschaften 88:351-354.
- 715 Ghiara G, Grande C, Ferrando S, Piccardo P (2018). The Influence of *Pseudomonas fluorescens* on
 716 Corrosion Products of Archaeological Tin-Bronze Analogues. JOM 70:81-85.
- 717 Giuffrida MG, Mazzoli R, Pessione E (2018). Back to the past. Decyphering cultural heritage secrets
 718 by protein identification. Appl Microbiol Biotechnol (In press)
- 719 Gtari M, Essoussi I, Maaoui R, Sghaier H, Boujmil R, Gury J, Pujic P, Brusetti L, Chouaia B, Crotti
 720 E, Daffonchio D, Boudabous A, Normand P (2012) Contrasted resistance of stone-dwelling
 721 Geodermatophilaceae species to stresses known to give rise to reactive oxygen species. FEMS
 722 Microbiol Ecol 80:566-577.
- 723 Gurtner C, Heyrman J, Piñar G, Lubitz W, Swings J, Rölleke S (2000). Comparative analyses of the
 724 bacterial diversity on two different biodeteriorated wall paintings by DGGE and 16S rDNA sequence
 725 analysis. Int Biodeterior Biodegrad 46:229-239.
- 726 Gutarowska B, Pietrzak K, Machnowski W, Miczarek JM (2017) Historical textiles – a review of
 727 microbial deterioration analysis and disinfection methods. Textile Research Journal 87:2388-2404.

- 728 Helms AC, Martiny AC, Hofman-Bang J, Ahring BK, Kilstrup M (2004). Identification of bacterial
729 cultures from archaeological wood using molecular biological techniques. *Int Biodeterior*
730 *Biodegradation* 53:79-88.
- 731 Heyrman J, Mergaert J, Denys R, Swings J (1999). The use of fatty acid methyl ester analysis (FAME)
732 for the identification of heterotrophic bacteria present on three mural paintings showing severe
733 damage by microorganisms. *FEMS Microbiology Letters* 181:55-62.
- 734 Imperi F, Caneva G, Cancellieri L, Ricci MA, Sodo A, Visca P (2007). The bacterial aetiology of
735 rosy discoloration of ancient wall paintings. *Environ microbiol* 9:2894-2902.
- 736 Jans MME, Nielsen-Marsh CM, Smith CI, Collins MJ, Kars H (2004). Characterisation of microbial
737 attack on archaeological bone. *J Archaeol Sci* 31:87-95.
- 738 Kehoe DM, Grossman AR (1994). Complementary chromatic adaptation: photoperception to gene
739 regulation. *Semin Cell Biol* 5:303-313.
- 740 Kendall C, Eriksen AMH, Kontopoulos I, Collins MJ, Turner-Walker G (2018). Diagenesis of
741 archaeological bone and tooth. *Palaeogeogr Palaeoclimatol Palaeoecol* 491:21-37.
- 742 Kip N, van Veen JA (2015). The dual role of microbes in corrosion. *ISME J* 9:542-51.
- 743 Krumbein WE, Urzì CE, Gehrman C (1991). Biocorrosion and biodeterioration of antique and
744 medieval glass. *Geomicrobiol J* 9:139-160.
- 745 Laiz L, Piñar G, Lubitz W, Saiz-Jimenez C (2003). Monitoring the colonization of monuments by
746 bacteria: cultivation versus molecular methods. *Environ Microbiol* 5:72-74.
- 747 Lamprinou V, Mammali M, Katsifas EA, Pantazidou AI, Karagouni AD (2013). Phenotypic and
748 molecular biological characterization of cyanobacteria from marble surfaces of treated and untreated
749 sites of Propylaea (Acropolis, Athens). *Geomicrobiol J* 30:371–378.
- 750 Landy ET, Mitchell JJ, Hotchkiss S, Eaton RA (2008). Bacterial diversity associated with
751 archaeological waterlogged wood: ribosomal RNA clone libraries and denaturing gradient gel
752 electrophoresis (DGGE). *Int Biodeterior Biodegradation* 61:106-116.

- 753 Lech T, Ziembinska-Buczynska A, Krupa N (2015). Analysis of microflora present on historical
754 textiles with the use of molecular techniques. *Int J Conserv Sci* 6:137–144.
- 755 Martino PD (2016). What About Biofilms on the Surface of Stone Monuments? *Open Conf Proced J*
756 7:14-28
- 757 Marty F, Gueuné H, Malard E, Sánchez-Amaya JM, Sjögren L, Abbas B, Muyzer G (2014).
758 Identification of key factors in accelerated low water corrosion through experimental simulation of
759 tidal conditions: influence of stimulated indigenous microbiota. *Biofouling* 30:281-297.
- 760 Marvasi M, Vedovato E, Balsamo C, Macherelli A, Dei L, Mastromei G, Perito B (2009). Bacterial
761 community analysis on the Mediaeval stained glass window “Natività” in the Florence Cathedral. *J*
762 *Cult Heritage* 10:124-133.
- 763 McCain JW, Mirocha CJ (1994). Screening computer diskettes and other magnetic media for
764 susceptibility to fungal colonization. *Int Biodeterior Biodegrad* 33:255-268.
- 765 McNamara CJ, Mitchell R (2005). Microbial deterioration of historic stone. *Front Ecol Environ*
766 3:445-451.
- 767 Milanesi C, Baldi F, Vignani R, Ciampolini F, Faleri C, Cresti M (2006). Fungal deterioration of
768 medieval wall fresco determined by analysing small fragments containing copper. *Int Biodeterior*
769 *Biodegrad* 57:7-13.
- 770 Neely AN, Maley MP (2000). Survival of enterococci and staphylococci on hospital fabrics and
771 plastic. *J Clin Microbiol* 38:724-726.
- 772 Nilsson T, Björdal C, Fällman E (2008). Culturing erosion bacteria: procedures for obtaining purer
773 cultures and pure strains. *Int Biodeterior Biodegradation* 61:17-23.
- 774 Oliveira VM, Lopes-Oliveira PF, Passarini MR, Menezes CB, Oliveira WR, Rocha AJ, Sette LD
775 (2011). Molecular analysis of microbial diversity in corrosion samples from energy transmission
776 towers. *Biofouling* 27:435-447.

- 777 Palla F, Mancuso FP, Billeci N (2013). Multiple approaches to identify bacteria in archaeological
778 waterlogged wood. *Journal of Cultural Heritage* 14:e61-e64.
- 779 Piccardo P, Mödlinger M, Ghiara G, Campodonico S, Bongiorno V (2013). Investigation on a
780 “tentacle-like” corrosion feature on Bronze Age tin-bronze objects. *Applied Physics A* 113:1039-
781 1047.
- 782 Pietrzak K, Puchalski M, Otlewska A, Wrzosek H, Guiamet P, Piotrowska M, Gutarowska B (2017).
783 Microbial diversity of pre-Columbian archaeological textiles and the effect of silver nanoparticles
784 misting disinfection. *J Cult Heritage* 23:138–147.
- 785 Poinar HN, Höss M, Bada JL, Pääbo S (1996). Amino acid racemization and the preservation of
786 ancient DNA. *Science* 272:864–866.
- 787 Prijambada ID, Negoro S, Yomo T, Urabe I (1995). Emergence of nylon oligomer degradation
788 enzymes in *Pseudomonas aeruginosa* PAO through experimental evolution. *Appl Environ Microbiol*
789 61:2020-202.
- 790 Radaelli A, Paganini M, Basavecchia V, Elli V, Neri M, Zanotto C, De Giuli Morghen C (2004).
791 Identification, molecular biotyping and ultrastructural studies of bacterial communities isolated from
792 two damaged frescoes of St Damian's Monastery in Assisi. *Lett Appl Microbiol* 38:447-453.
- 793 Rémazeilles C, Dheilly A, Sable S, Lanneluc I, Neff D, Refait P (2010a). Microbiologically
794 influenced corrosion process of archaeological iron nails from the sixteenth century. *Corros Eng Sci*
795 *Technol* 45:388-394.
- 796 Rémazeilles C, Saheb M, Neff D, Guilminot E, Tran K, Bourdoiseau JA, Sabot R, Jeannin M,
797 Matthiesen H, Dillmann P, Refait P (2010b). Microbiologically influenced corrosion of
798 archaeological artefacts: characterisation of iron(II) sulfides by Raman spectroscopy. *J Raman*
799 *Spectrosc* 41:1425–1433.
- 800 Rölleke S, Muyzer G, Wawer C, Wanner G, Lubitz W (1996). Identification of bacteria in a
801 biodegraded wall painting by denaturing gradient gel electrophoresis of PCR-amplified gene
802 fragments coding for 16S rRNA. *Appl Environ Microbiol* 62:2059-2065.

- 803 Rowe L, Howard GT (2002) Growth of *Bacillus subtilis* on polyurethane and the purification and
804 characterization of a polyurethanase-lipase enzyme. *Int Biodeterior Biodegrad* 50:33-40.
- 805 Saarela M, Alakomi HL, Suihko ML, Maunuksela L, Raaska L, Mattila-Sandholm T (2004).
806 Heterotrophic microorganisms in air and biofilm samples from Roman catacombs, with special
807 emphasis on actinobacteria and fungi. *Int Biodeterior Biodegrad* 54:27-37.
- 808 Sakai K, Yamauchi T, Nakasu F, Ohe T (1996). Biodegradation of cellulose acetate by *Neisseria*
809 *sicca*. *Biosci Biotechnol Biochem* 60:1617-1622.
- 810 Sclocchi MC, Damiano E, Matè D, Colaizzi P, Pinzari F (2013). Fungal biosorption of silver particles
811 on 20th-century photographic documents. *Int Biodeterior Biodegrad* 84:367-371.
- 812 Seal KJ (1988). The biodegradation of naturally occurring and synthetic plastic polymers. *Biodeterior*
813 *Abstracts* 2:296–317.
- 814 Seves A, Romano M., Maifreni T, Sora S, Ciferri O (1998). The microbial degradation of silk: a
815 laboratory investigation. *Int Biodeterior Biodegrad* 42:203–211.
- 816 Singh AP (2012). A review of microbial decay types found in wooden objects of cultural heritage
817 recovered from buried and waterlogged environments. *J Cult Herit* 13:S16-S20.
- 818 Sterflinger K (2010). Fungi: Their Role in Deterioration of Cultural Heritage. *Fungal Biol Rev* 24:47–
819 55.
- 820 Szostak-Kotow J (2004). Biodeterioration of textiles. *Int Biodeterior Biodegrad* 53:165-170.
- 821 Videla HA, Herrera LK (2005). Microbiologically influenced corrosion: looking to the future. *Int*
822 *Microbiol.* 8:169-80.
- 823 Villa F, Pitts B, Lauchnor E, Cappitelli F, Stewart PS (2015). Development of a Laboratory Model
824 of a Phototroph-Heterotroph Mixed-Species Biofilm at the Stone/Air Interface. *Front Microbiol*
825 6:1251.

- 826 Violetta MR, Mazzoli R, Barello C, Fattori P, Giuffrida M.G, Pessione E (2014). Combining LC-
827 MS/MS, PMF and N-terminal amino acid sequencing for multiplexed characterization of a bacterial
828 surfactant glycoprotein biosynthesized by *Acinetobacter radioresistens* S13. RSC Adv. 4:10918-
829 10927.
- 830 Wadsworth C, Procopio N, Anderung C, Carretero JM, Iriarte E, Valdiosera C, Elburg R, Penkman
831 K, Buckley M (2017). Comparing ancient DNA survival and proteome content in 69 archaeological
832 cattle tooth and bone samples from multiple European sites. J Proteomics 158:1-8.
- 833 Webb JS, Nixon M, Eastwood IM, Greenhalgh M, Robson GD, Handley PS (2000). Fungal
834 colonization and biodeterioration of plasticized polyvinyl chloride. Appl Environ Microbiol 66:3194-
835 3200.
- 836 Yoshida S, Hiraga K, Takehana T, Taniguchi I, Yamaji H, Maeda Y, Toyohara K, Miyamoto K,
837 Kimura Y, Oda K (2016) A bacterium that degrades and assimilates poly(ethylene terephthalate).
838 Science 351:1196-1199.
- 839

840 **Figure Legend**

841 Fig. 1. Oseberg Viking ship exposed in the Viking Ship Museum at Bygdøy in Oslo (Norway).

842 Fig. 2. Schematic representation of three commonly used molecular-based procedures for bacteria
843 identification in cultural heritage samples. a) Denaturing Gel Gradient Electrophoresis (DGGE); b)
844 Restriction Fragment Length Polymorphism (RFLP); c) Fatty Acid Methyl Esther Analysis (FAME).

845 Fig. 3. Bacterioruberin pigments (a) produced by bacterial cultures of *Rubrobacter radiotolerans* (b)
846 and which contaminate the 9th century frescoes of the Crypt of the Original Sin Chapel near Matera
847 (Italy) (c).

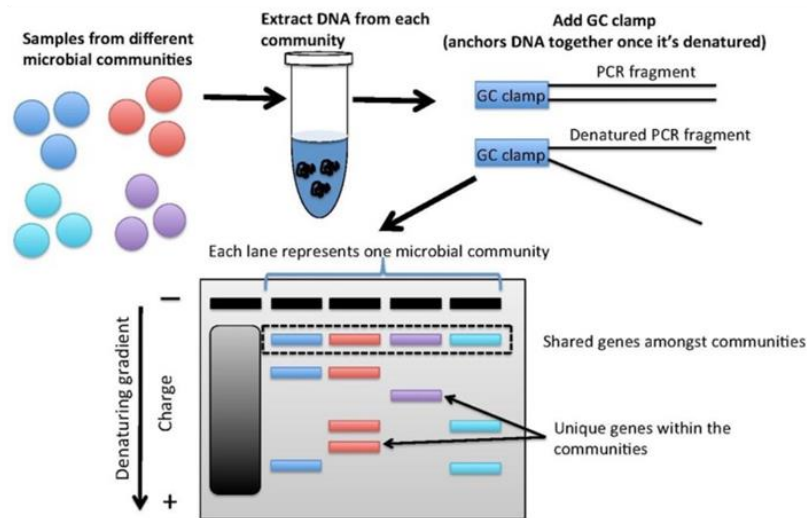
848 Fig. 4. Black and white and color photographic films at risk to microbial deterioration.

849 Fig. 5. Apollo spacesuit on which fungal contamination has been ascertained.

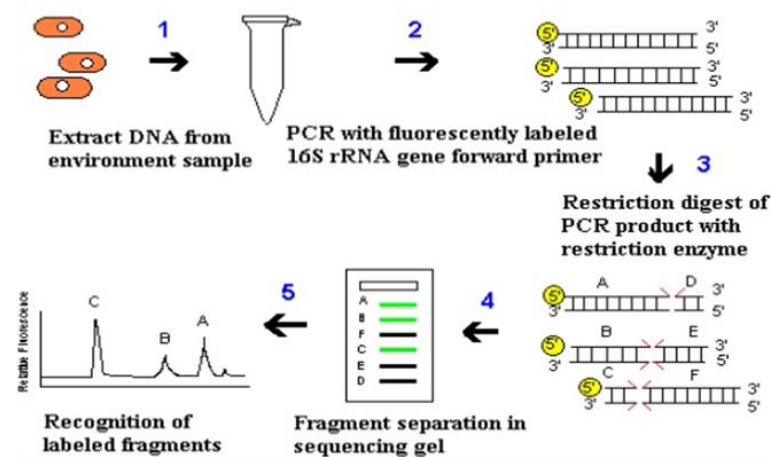


850 Fig. 1

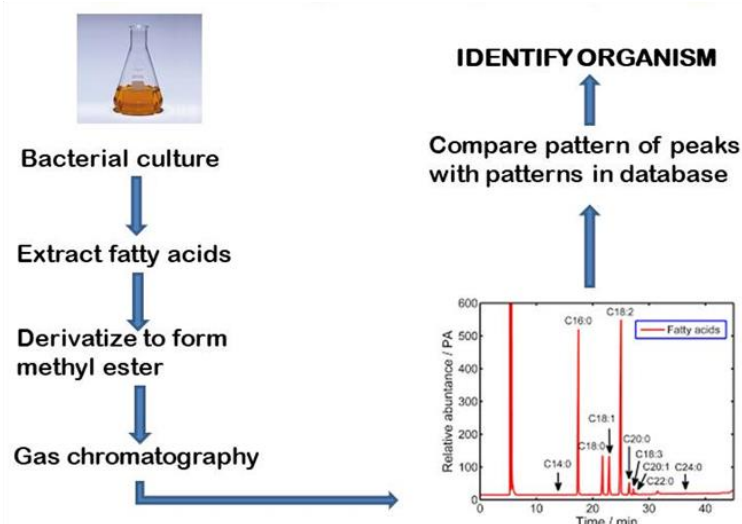
a Denaturing Gel Gradient Electrophoresis (DGGE)



b Restriction Fragment Length Polymorphism (RFLP)



c Fatty Acid Methyl Ester (FAME) Analysis



852 Fig. 3

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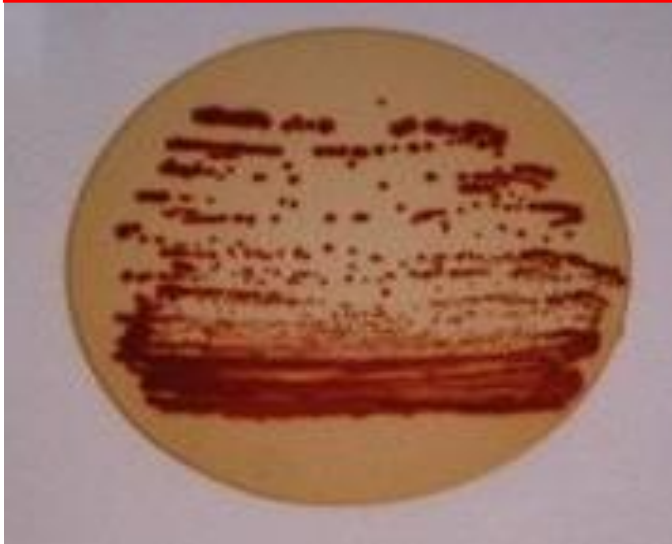
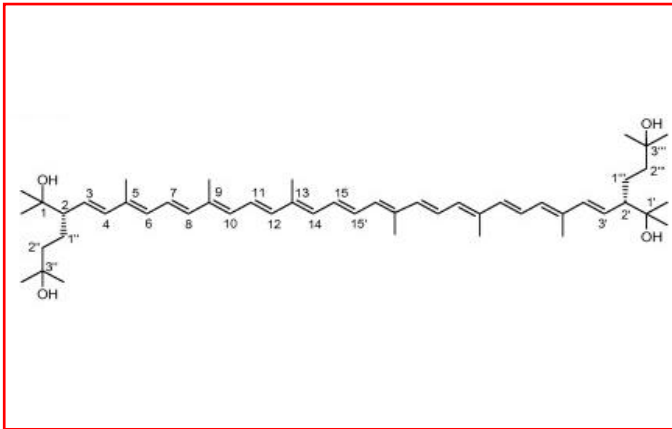
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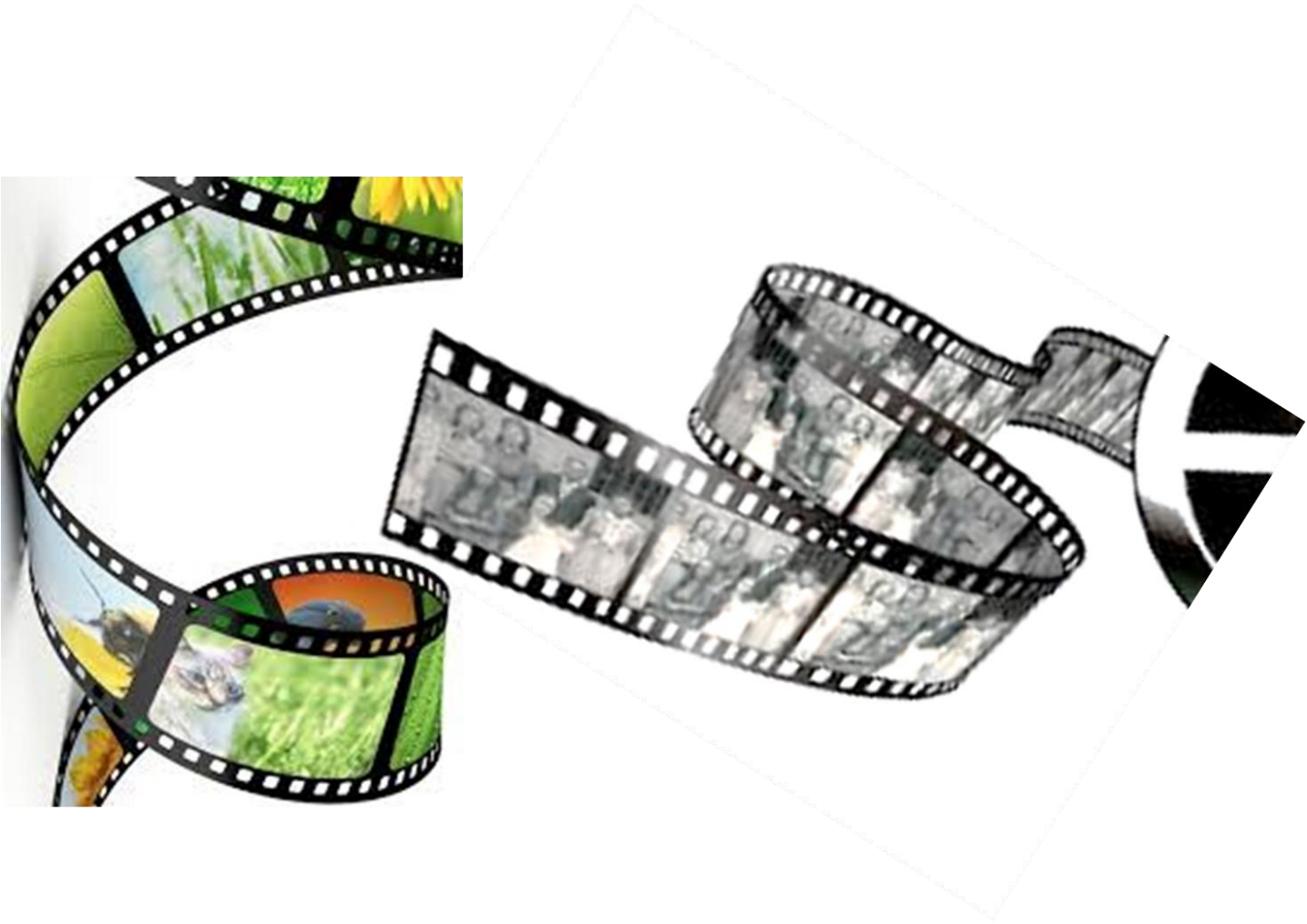
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863 Fig. 4



865 Fig. 5

